

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 08/485,943B  
Source: JFW16  
Date Processed by STIC: 10/11/2005

***ENTERED***

CRF Errors Edited by the ST-10 Systems Branch

Serial Number:

08/485,943B

CRF Edit Date:

10/11/2005

Edited by: DA

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

— Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

— Other:

*Corrected Seq ID 99 for  
numeric identifier <400>*

Revised 09/09/2003



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/485,943B

DATE: 10/11/2005

TIME: 14:25:33

Input Set : A:\PTO.da.txt

Output Set: N:\CRF4\10112005\H485943B.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: THE ROCKEFELLER UNIVERSITY

8 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
9 ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES

THEREOF

11 (iii) NUMBER OF SEQUENCES: 100

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Klauber &amp; Jackson

15 (B) STREET: 411 Hackensack Avenue

16 (C) CITY: Hackensack

17 (D) STATE: New Jersey

18 (E) COUNTRY: USA

19 (F) ZIP: 07601

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/08/485,943B

C--&gt; 29 (B) FILING DATE: 07-Jun-1995

W--&gt; 45 (C) CLASSIFICATION:

42 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/438,431

34 (B) FILING DATE: May 10, 1995

38 (A) APPLICATION NUMBER: 08/347,563

39 (B) FILING DATE: November 30, 1994

43 (A) APPLICATION NUMBER: 08/292,345

44 (B) FILING DATE: August 17, 1994

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: Jackson Esq., David A.

49 (B) REGISTRATION NUMBER: 26,742

50 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: 201 487-5800

54 (B) TELEFAX: 201 343-1684

55 (C) TELEX: 133521

57 (2) INFORMATION FOR SEQ ID NO: 1:

59 (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 2793 base pairs

61 (B) TYPE: nucleic acid

62 (C) STRANDEDNESS: double

63 (D) TOPOLOGY: linear

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Input Set : A:\PTO.da.txt

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65 (ii) MOLECULE TYPE: DNA (genomic)  
 66 (A) DESCRIPTION: Murine ob cDNA  
 68 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 72 (vi) ORIGINAL SOURCE:  
 73 (A) ORGANISM: Murine  
 75 (ix) FEATURE:  
 76 (A) NAME/KEY: CDS  
 77 (B) LOCATION: 57..560  
 80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 82 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA 56  
 84 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG 104  
 85 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu  
 86 1 5 10 15  
 88 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA 152  
 89 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys  
 90 20 25 30  
 92 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG 200  
 93 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr  
 94 35 40 45  
 96 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT 248  
 97 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro  
 98 50 55 60  
 100 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA 296  
 101 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala  
 102 65 70 75 80  
 104 GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG 344  
 105 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln  
 106 85 90 95  
 108 ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC 392  
 109 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Ala  
 110 100 105 110  
 112 TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA 440  
 113 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro  
 114 115 120 125  
 116 GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG 488  
 117 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val  
 118 130 135 140  
 120 GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG 536  
 121 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln  
 122 145 150 155 160  
 124 TTG GAT GTT AGC CCT GAA TGC TGA AGTTCAAAG GCCACCAGGC TCCCAAGA 588  
 125 Leu Asp Val Ser Pro Glu Cys \*  
 126 165  
 128 ATCATGTAGA GGGAAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC 648  
 130 ACACATCCAT CATTCAATTTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA 708  
 132 CAATGCTTGA CTCAAGTTAT CCACACAACT TCATGAGCAC AAGGAGGGC CAGCCTGCAG 768  
 134 AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG 828  
 136 TCCCACCTGC TCCGGGTACA TGTTCTCCG TGGGTACACG CTTCGCTGCG GCCCAGGAGA 888

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138	GGTGAGGTAG	GGATGGGTAG	AGCCTTTGGG	CTGTCTCAGA	GTCTTTGGGA	GCACCGTGAA	948
140	GGCTGCATCC	ACACACAGCT	GGAAACTCCC	AAGCAGCACA	CGATGGAAGC	ACTTATTTAT	1008
142	TTATTCTGCA	TTCTATTTG	GATGGATCTG	AAGCAAGGC	TCAGCTTTT	CAGGCTTTGG	1068
144	GGGTCAAGCCA	GGATGAGGAA	GGCTCCTGGG	GTGCTGCTT	CAATCCTATT	GATGGGTCTG	1128
146	CCCGAGGCAA	ACCTAATTTT	TGAGTGACTG	GAAGGAAGGT	TGGGATCTTC	CAAACAAGAG	1188
148	TCTATGCAGG	TAGCGCTCAA	GATTGACCTC	TGGTACTGG	TTTGTTTCT	ATTGTGACTG	1248
150	ACTCTATCCA	AACACGTTG	CAGCGGCATT	GCCGGGAGCA	TAGGCTAGGT	TATTATCAAA	1308
152	ACGAGATGAA	TTTTGTCAAG	TGTAATATGT	ATCTATGTGC	ACCTGAGGGT	AGAGGATGTG	1368
154	TTAGAGGGAG	GGTGAAGGAT	CCGGAAGTGT	TCTCTGAATT	ACATATGTGT	GGTAGGCTTT	1428
156	TCTGAAAGGG	TGAGGCATT	TCTTACCTCT	GTGGCCACAT	AGTGTGGCTT	TGTAAAAGG	1488
158	ACAAAGGAGT	TGACTCTTTC	CGGAACATT	GGAGTGTACC	AGGCACCCTT	GGAGGGGCTA	1548
160	AAGCTACAGG	CCTTTGTTG	GCATATTGCT	GAGCTCAGGG	AGTGAGGGCC	CCACATTTGA	1608
162	GACAGTGAGC	CCCAAGAAAA	GGGTCCCTGG	TGTAGATCTC	CAAGGTTGTC	CAGGGTTGAT	1668
164	CTCACAATGC	TTTCTTAAG	CAGGTAGACG	TTTGCATGCC	AATATGTGGT	TCTCATCTGA	1728
166	TTGGTTCATC	CAAAGTAGAA	CCCTGTCTCC	CACCCATTCT	GTGGGGAGTT	TTGTTCCAGT	1788
168	GGGAATGAGA	AATCACTTAG	CAGATGGTCC	TGAGCCCTGG	GCCAGCACTG	CTGAGGAAGT	1848
170	GCCAGGGCCC	CAGGCCAGGC	TGCCAGAATT	GCCCTTCGGG	CTGGAGGATG	AACAAAGGGG	1908
172	CTTGGGTTTT	TCCATCACCC	CTGCACCCCTA	TGTACCCATC	AAACTGGGG	GCAGATCAGT	1968
174	GAGAGGACAC	TTGATGGAAA	GCAATACACT	TTAAGACTGA	GCACAGTTTC	GTGCTCAGCT	2028
176	CTGTCTGGTG	CTGTGAGCTA	GAGAAGCTCA	CCACATACAT	ATAAAAATCA	GAGGCTCATG	2088
178	TCCCTGTGGT	TAGACCCCTAC	TCGCGGCGGT	GTACTCCACC	ACAGCAGCAC	CGCACCGCTG	2148
180	GAAGTACAGT	GCTGCTTCA	ACAGGTGTGA	AAGAACCTGA	GCTGAGGGTG	ACAGTGCCA	2208
182	GGGGAACCC	GCTTGAGTC	TATTGCATT	ACATACCGCA	TTTCAGGGCA	CATTAGCATE	2268
184	CACTCCTATG	GTAGCACACT	GTTGACAATA	GGACAAGGG	TAGGGGTTGA	CTATCCCTTA	2328
186	TCCAAAATGC	TTGGGACTAG	AAGAGTTTG	GATTAGAG	TCTTTTCAGG	CATAGGTATA	2388
188	TTTGAGTATA	TATAAAATGA	GATATCTTGG	GGATGGGGCC	CAAGTATAAA	CATGAAGTTC	2448
190	ATTTATATT	CATAATACCG	TATAGACACT	GCTTGAAGTG	TAGTTTATA	CAGTGTGTTA	2508
192	ATAAACGTTG	TATGCATGAA	AGACGTTTT	ACAGCATGAA	CCTGTCTACT	CATGCCAGCA	2568
194	CTCAAAATACC	TTGGGGTTTT	GGAGCAGTT	GGATCTGGG	TTTTCTGTTA	AGAGATGGTT	2628
196	AGCTTATACC	AAAACCATA	ATGGCAAACA	GGCTGCAGGA	CCAGACTGGA	TCCTCAGCCC	2688
198	TGAAGTGTGC	CCTTCAGCC	AGGTCATACC	CTGTGGAGGT	GAGCAGGATC	AGGTTTTGTG	2748
200	GTGCTAAGAG	AGGAGTTGGA	GGTAGATT	GGAGGATCTG	AGGGC		2793

203 (2) INFORMATION FOR SEQ ID NO: 2:

205 (i) SEQUENCE CHARACTERISTICS:

206 (A) LENGTH: 167 amino acids

207 (B) TYPE: amino acid

208 (D) TOPOLOGY: linear

210 (ii) MOLECULE TYPE: protein

211 (A) DESCRIPTION: Murine ob polypeptide

213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

215	Met	Cys	Trp	Arg	Pro	Leu	Cys	Arg	Phe	Leu	Trp	Leu	Trp	Ser	Tyr	Leu	
216	1					5				10				15			
218	Ser	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	
219								20		25			30				
221	Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	
222								35		40			45				
224	Gln	Ser	Val	Ser	Ala	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	
225								50		55			60				
227	Gly	Leu	His	Pro	Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	

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228	65	70	75	80
230	Val	Tyr	Gln	Gln
231	Val	Leu	Thr	Ser
232	Asn	Asn	Asp	Glu
233	Ile	Ala	Asn	Asp
234	Leu	Glu	Asn	Leu
235	Arg	Arg	Asp	Leu
236	Leu	His	Leu	Leu
237	Leu	Gln	Leu	Gln
238	Thr	Ser	Gly	Lys
239	Glu	Ser	Leu	Asp
240	Val	Leu	Gly	Val
241	Asp	Glu	Ala	Ser
242	Leu	Tyr	Ser	Thr
243	Val	Leu	Gly	Gly
244	Ala	Ser	Leu	Asp
245	Arg	Gln	Gln	Ile
246	Leu	Gln	Asp	Leu
247	Asp	Asp	Ile	Gln
248	Val	Ser	Leu	Gln
249	Pro	Glu	Gly	160
250	Cys			
251	165			

## 249 (2) INFORMATION FOR SEQ ID NO: 3:

251	(i) SEQUENCE CHARACTERISTICS:
252	(A) LENGTH: 700 base pairs
253	(B) TYPE: nucleic acid
254	(C) STRANDEDNESS: double
255	(D) TOPOLOGY: linear
256	(ii) MOLECULE TYPE: cDNA
257	(A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
258	(iii) HYPOTHETICAL: NO
259	(iv) ANTI-SENSE: NO
260	(vi) ORIGINAL SOURCE:
261	(A) ORGANISM: Human
262	(ix) FEATURE:
263	(A) NAME/KEY: CDS
264	(B) LOCATION: 46..546
265	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

266	NNNGNNNTTG CAAGGCCAA GAAGCCANN NTCCTGGGAA GGAAA ATG CAT TGG	54
267	Met His Trp	
268	1	
269	GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC	102
270	Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val	
271	5 10 15	
272	CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC	150
273	Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile	
274	20 25 30 35	
275	AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC	198
276	Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val	
277	40 45 50	
278	TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC	246
279	Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His	
280	55 60 65	
281	CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA	294
282	Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln	
283	70 75 80	
284	CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC	342
285	Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn	

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300	85	90	95														
302	GAC	CTG	GAG	AAC	CTC	CGG	GAT	CTT	CTT	CAC	GTG	CTG	GCC	TTC	TCT	AAG	390
303	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	Phe	Ser	Lys	
304	100				105					110				115			
306	AGC	TGC	CAC	TTG	CCC	TGG	GCC	AGT	GGC	CTG	GAG	ACC	TTG	GAC	AGC	CTG	438
307	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	Asp	Ser	Leu	
308					120				125				130				
310	GGG	GGT	GTC	CTG	GAA	GCT	TCA	GGC	TAC	TCC	ACA	GAG	GTG	GTG	GCC	CTG	486
311	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	
312					135				140			145					
314	AGC	AGG	CTG	CAG	GGG	TCT	CTG	CAG	GAC	ATG	CTG	TGG	CAG	CTG	GAC	CTC	534
315	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	Leu	Asp	Leu	
316					150			155			160						
318	AGC	CCT	GGG	TGC	TGAGGCCTT	GAAGGTCACT	CTTCCTGCAA	GGACTNACGT									585
319	Ser	Pro	Gly	Cys													
320		165															
322	TAAGGGAAGG	AACTCTGGTT	TCCAGGTATC	TCCAGGATTG	AAGAGCATTG	CATGGACACC											645
324	CCTTATCCAG	GACTCTGTCA	ATTTCCCTGA	CTCCTCTAAG	CCACTCTTCC	AAAGG											700
327	(2)	INFORMATION FOR SEQ ID NO: 4:															
329	(i)	SEQUENCE CHARACTERISTICS:															
330		(A)	LENGTH:	167	amino acids												
331		(B)	TYPE:	amino acid													
332		(D)	TOPOLOGY:	linear													
334	(ii)	MOLECULE TYPE:	protein														
335		(A)	DESCRIPTION:	Human ob polypeptide													
337	(vi)	ORIGINAL SOURCE:															
339	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:															
341	Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu	
342	1				5				10			15					
344	Phe	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	
345					20				25			30					
347	Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	
348					35			40			45						
350	Gln	Ser	Val	Ser	Ser	Lys	Gln	Lys	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	
351					50			55			60						
353	Gly	Leu	His	Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	
354					65			70			75			80			
356	Val	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Ile	Gln	
357					85				90			95					
359	Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	
360					100				105			110					
363	Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	
364					115			120			125						
367	Asp	Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	
368					130			135			140						
370	Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	
371					145			150			155			160			
374	Leu	Asp	Leu	Ser	Pro	Gly	Cys										
375					165												

## VERIFICATION SUMMARY

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DATE: 10/11/2005

TIME: 14:25:34

Input Set : A:\PTO.da.txt

Output Set: N:\CRF4\10112005\H485943B.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:40 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:45 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:436 M:220 C: Keyword misspelled or invalid format, [(A) DESCRIPTION:]  
L:509 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
L:673 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:695 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
L:717 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16  
L:830 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21  
L:1128 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29  
L:1148 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30  
L:1170 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31  
L:1192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32  
L:1214 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33  
L:1234 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34  
L:1255 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35  
L:1276 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36  
L:1297 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37  
L:1339 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39  
L:1362 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40  
L:1385 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41  
L:1407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42  
L:1430 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43  
L:1453 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44  
L:1474 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45  
L:1496 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46  
L:1519 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47  
L:1541 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48  
L:1564 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49  
L:1587 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50  
L:1610 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51  
L:1633 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52  
L:1655 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=53  
L:1678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=54  
L:1701 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=55  
L:1724 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=56  
L:1747 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=57  
L:1770 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=58  
L:1793 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=59  
L:1816 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=60  
L:1839 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=61  
L:1862 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=62  
L:1885 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=63

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Input Set : A:\PTO.da.txt

Output Set: N:\CRF4\10112005\H485943B.raw

L:1907 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=64  
L:1930 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=65  
L:1953 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=66  
L:1977 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=67  
L:2000 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=68  
L:2021 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=69  
L:2044 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=70  
L:2067 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=71  
L:2090 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=72  
L:2113 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=73  
L:2136 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=74

**Raw Sequence Listing before editing,  
for reference only**



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/08/485,943B

DATE: 10/05/2005  
TIME: 11:48:22

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\10052005\H485943B.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: THE ROCKEFELLER UNIVERSITY  
8 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
9 ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES

THEREOF

11 (iii) NUMBER OF SEQUENCES: 100

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Klauber & Jackson  
15 (B) STREET: 411 Hackensack Avenue  
16 (C) CITY: Hackensack  
17 (D) STATE: New Jersey  
18 (E) COUNTRY: USA  
19 (F) ZIP: 07601

Does Not Comply  
Corrected Diskette Needed

(Pg-2)

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/08/485,943B  
29 (B) FILING DATE: 07-Jun-1995

W--&gt; 45 (C) CLASSIFICATION:

42 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/438,431  
34 (B) FILING DATE: May 10, 1995  
38 (A) APPLICATION NUMBER: 08/347,563  
39 (B) FILING DATE: November 30, 1994  
43 (A) APPLICATION NUMBER: 08/292,345  
44 (B) FILING DATE: August 17, 1994

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: Jackson Esq., David A.  
49 (B) REGISTRATION NUMBER: 26,742  
50 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: 201 487-5800  
54 (B) TELEFAX: 201 343-1684  
55 (C) TELEX: 133521

## ERRORED SEQUENCES

2828 (2) INFORMATION FOR SEQ ID NO: 99:  
2830 (i) SEQUENCE CHARACTERISTICS:

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/485,943B

DATE: 10/05/2005

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Input Set : A:\PTO.RJ.txt

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2831 (A) LENGTH: 20 amino acids  
2832 (B) TYPE: amino acid  
2833 (D) TOPOLOGY: linear  
2835 (ii) MOLECULE TYPE: peptide 99  
2837 (v) FRAGMENT TYPE: N-terminal  
E--> 2840 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98  
2842 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
2843 1 5 10 15  
2845 Arg Gly Ser Pro  
2846 20

VERIFICATION SUMMARY  
PATENT APPLICATION: US/08/485,943B

DATE: 10/05/2005  
TIME: 11:48:23

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\10052005\H485943B.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)  
 L:40 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)  
 L:45 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)  
 L:436 M:220 C: Keyword misspelled or invalid format, [(A) DESCRIPTION:]  
 L:509 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
 L:529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
 L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
 L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
 L:673 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
 L:695 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
 L:717 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16  
 L:830 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21  
 L:1128 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29  
 L:1148 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30  
 L:1170 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31  
 L:1192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32  
 L:1214 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33  
 L:1234 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34  
 L:1255 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35  
 L:1276 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36  
 L:1297 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37  
 L:1339 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39  
 L:1362 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40  
 L:1385 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41  
 L:1407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42  
 L:1430 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43  
 L:1453 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44  
 L:1474 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45  
 L:1496 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46  
 L:1519 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47  
 L:1541 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48  
 L:1564 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49  
 L:1587 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50  
 L:1610 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51  
 L:1633 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52  
 L:1655 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=53  
 L:1678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=54  
 L:1701 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=55  
 L:1724 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=56  
 L:1747 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=57  
 L:1770 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=58  
 L:1793 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=59  
 L:1816 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=60  
 L:1839 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=61  
 L:1862 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=62  
 L:1885 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=63

## VERIFICATION SUMMARY

PATENT APPLICATION: US/08/485,943B

DATE: 10/05/2005

TIME: 11:48:23

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10052005\H485943B.raw

L:1907 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=64  
L:1930 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=65  
L:1953 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=66  
L:1977 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=67  
L:2000 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=68  
L:2021 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=69  
L:2044 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=70  
L:2067 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=71  
L:2090 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=72  
L:2113 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=73  
L:2136 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=74  
L:2840 M:212 E: (34) Invalid or duplicate Sequence ID Number, Value=[98:]